

Plant per-amino acid GC3 vs GC3 graphs

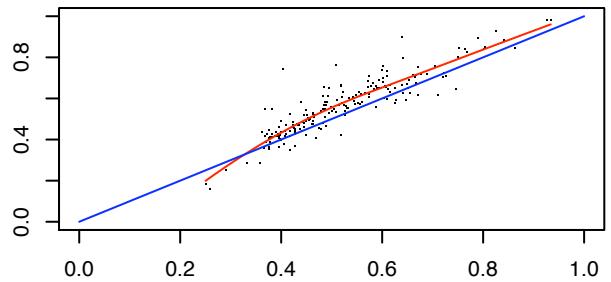
Supplemental data for the publication Palidwor et al, 2010

The x-axis of each graph is GC3, the y-axis is codon frequency (per-amino acid) for plant genomes based on the gbpln.spsum CUTG codon usage data derived from the NCBI GenBank Flat File Release 160.0.

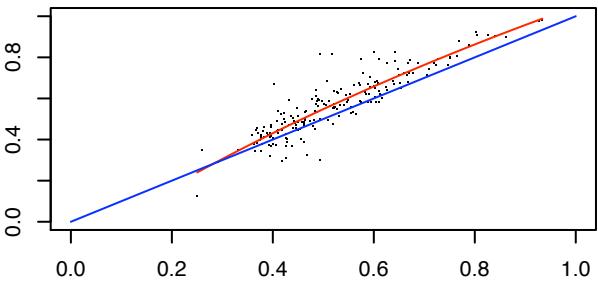
The x-axis of each graph is GC3, the y-axis is codon frequency (per-amino acid). Each point represents a single plant genome.

The blue line is the model prediction, the red line a loess fit to the observed data.

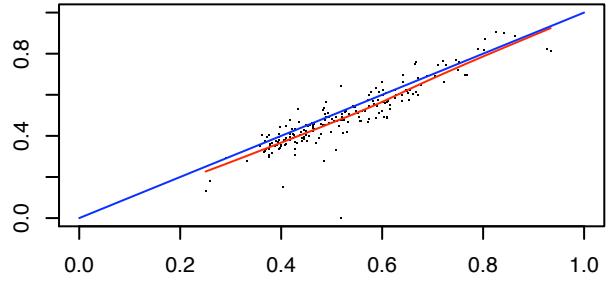
phe (GC3)



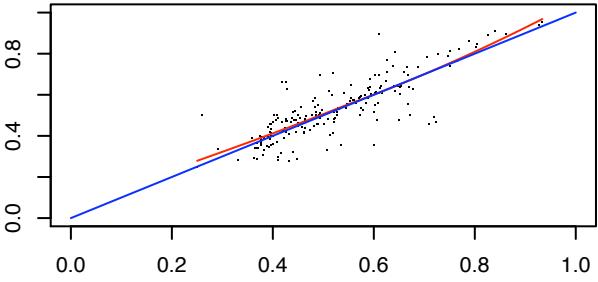
tyr (GC3)



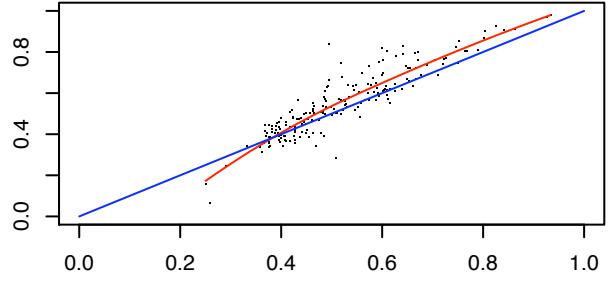
his (GC3)



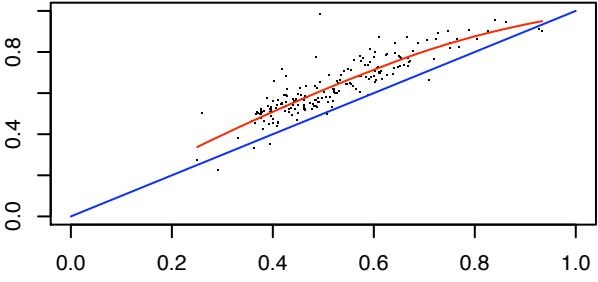
gln (GC3)



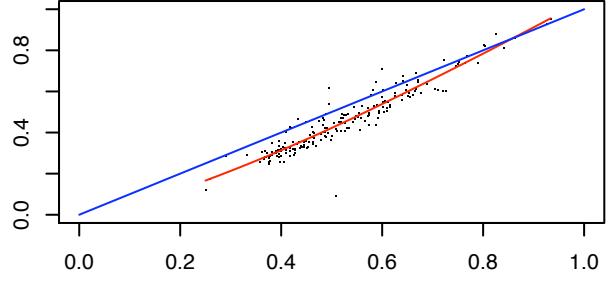
asn (GC3)



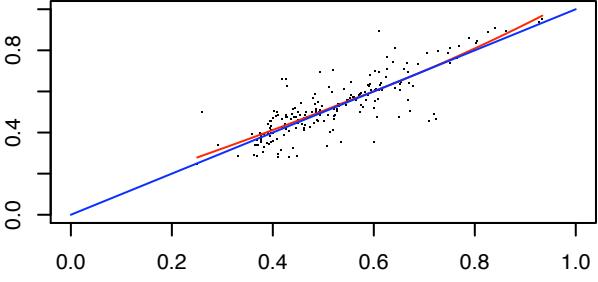
lys (GC3)

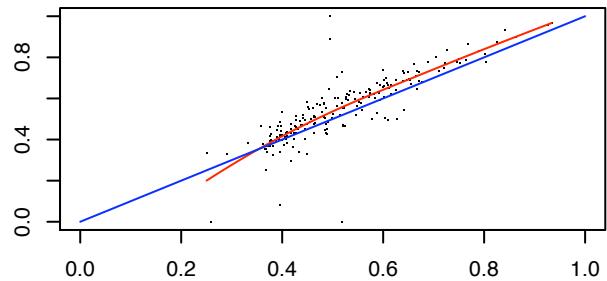
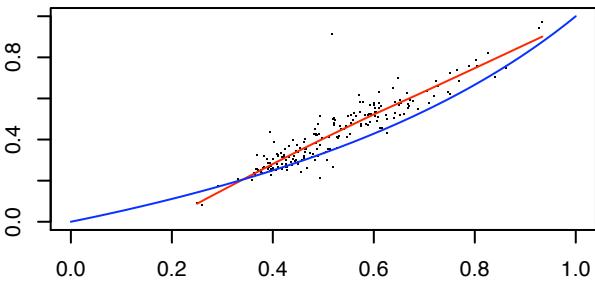
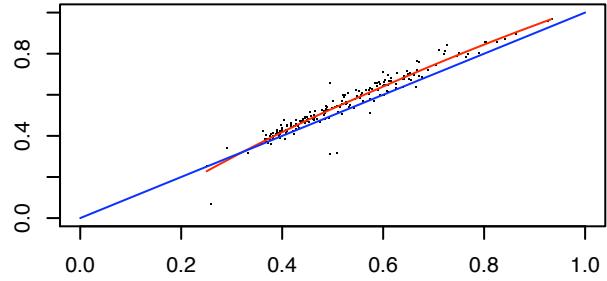
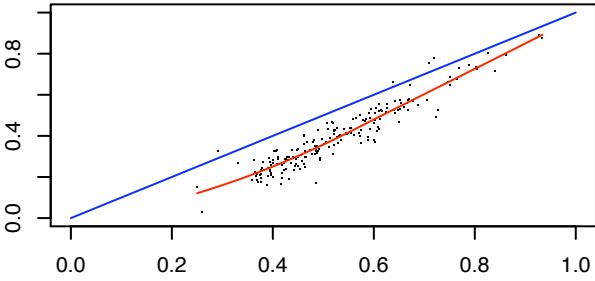
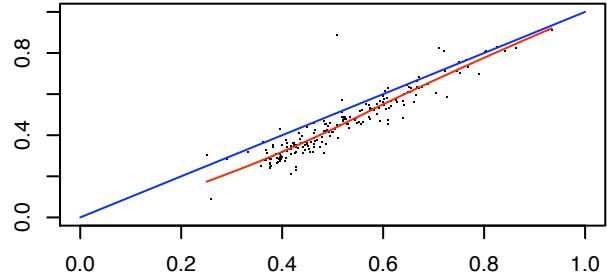
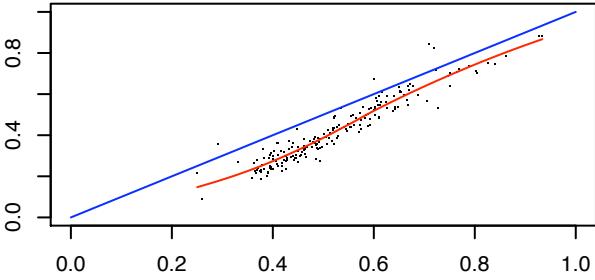
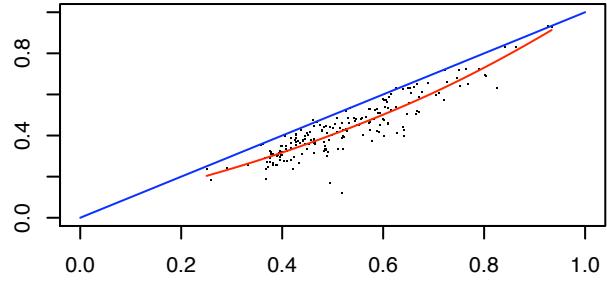
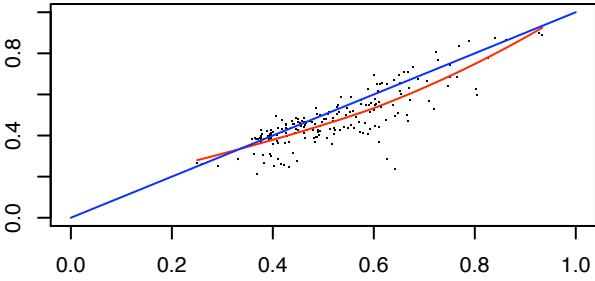


asp (GC3)

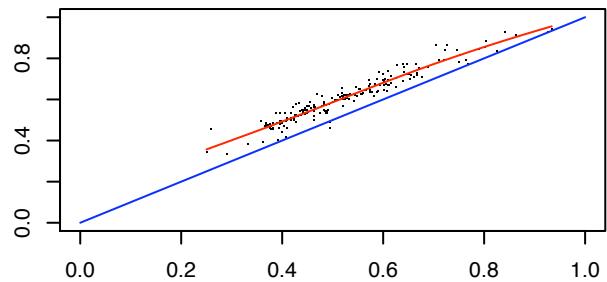


glu (GC3)

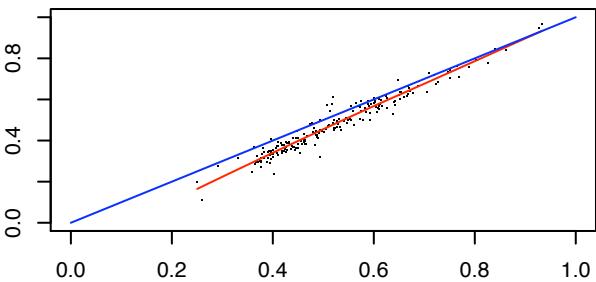


cys (GC3)**ile (GC3)****val (GC3)****pro (GC3)****thr (GC3)****ala (GC3)****gly (GC3)****arg (GC3)**

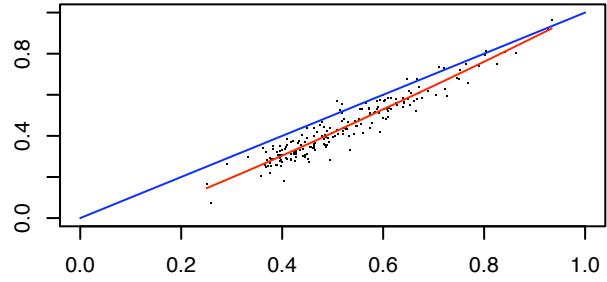
leu (GC3)



ser (GC3)



ser4 (GC3)



ser2 (GC3)

